

# SEQUENCE SEARCH SUMMARY

10/6/6309

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 15, 2005, 11:20:25 ; Search time 558 Seconds  
(without alignments)  
10152.675 Million cell updates/sec

Title: US-10-616-309-3  
Perfect score: 957  
Sequence: 1 atgaagcaacttttggtttgc.....agttcggggcagcgcaatga 957

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:\*

- 1: geneseqn1980s:\*
- 2: geneseqn1990s:\*
- 3: geneseqn2000s:\*
- 4: geneseqn2001as:\*
- 5: geneseqn2001bs:\*
- 6: geneseqn2002as:\*
- 7: geneseqn2002bs:\*
- 8: geneseqn2003as:\*
- 9: geneseqn2003bs:\*
- 10: geneseqn2003cs:\*
- 11: geneseqn2003ds:\*
- 12: geneseqn2004as:\*
- 13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	957	100.0	957	12 ADH45224	Adh45224 Enterobac
2	638.8	66.8	1122	3 AAZ98342	Aaz98342 A. thalia
3	556.8	58.2	1041	11 ACH98809	Ach98809 Klebsiell
4	501.4	52.4	1968	5 AAS82067	Aas82067 DNA encod

in Ecol. →  
6610836

ADP1  
W/O 2100  
PF 1100 PD 03  
A-L

year only  
6610836

	5	257.8	26.9	957	10	ACF71993	ACf71993 Photorhab
	6	257.8	26.9	110000	10	ACF67367_51	Continuation (52 o
	7	257.8	26.9	110000	10	ACF67367_52	Continuation (53 o
	8	257.8	26.9	110000	10	ACF65387_3	Continuation (4 of
	9	191.2	20.0	1020	10	ADF03160	Adf03160 Bacterial
c	10	174.4	18.2	1986	5	AAS92912	Aas92912 DNA encod
c	11	174.4	18.2	2180	5	AAS93271	Aas93271 DNA encod
	12	136.6	14.3	106645	13	ADT05645	Adt05645 Haemophil
	13	136.6	14.3	110000	2	AAT42063_06	Continuation (7 of
	14	100	10.4	100	8	ACD79770	Acd79770 E. coli K
	15	100	10.4	100	8	ACD79771	Acd79771 E. coli K
	16	100	10.4	100	8	ACD79772	Acd79772 E. coli K
c	17	74	7.7	1855	13	ADT05072	Adt05072 Haemophil
c	18	43.2	4.5	2000	8	ADA71938	Ada71938 Rice gene
	19	42.2	4.4	2000	8	ADA71938	Ada71938 Rice gene
c	20	42	4.4	4590	5	AAH24065	Aah24065 Yeast AOD
	21	38	4.0	951	13	ADS60284	Ads60284 Bacterial
c	22	37.8	3.9	763	13	ADS62580	Ads62580 Bacterial
c	23	37.8	3.9	763	13	ADS59814	Ads59814 Bacterial
	24	37.6	3.9	1800	2	AAQ70238	Aaq70238 P. aerugi
	25	37.6	3.9	1800	2	AAQ70237	Aaq70237 P. aerugi
	26	37.6	3.9	1800	3	AAA51920	Aaa51920 P. aerugi
	27	36	3.8	1065	11	ABD14466	Abd14466 Pseudomon
c	28	36	3.8	1308	11	ABD14265	Abd14265 Pseudomon
	29	35.8	3.7	349980	5	AAH68526	Aah68526 C glutami
	30	34.8	3.6	2954	4	AAK91223	Aak91223 Human dig
c	31	34.4	3.6	79256	13	ABD33177	Abd33177 Murine ca
	32	34.2	3.6	421	9	ACH30553	Ach30553 Human tes
	33	34.2	3.6	110000	13	ABD32721_1	Continuation (2 of
c	34	33.6	3.5	168407	13	ABD33266	Abd33266 Murine ca
	35	33.4	3.5	349980	6	ABQ81845	Abq81845 Bifidobac
c	36	33.2	3.5	317	13	ADR60190	Adr60190 Cotton cD
	37	33.2	3.5	1554	13	ADR03666	Adr03666 Aplysia p
c	38	33.2	3.5	1882	2	AAT59768	Aat59768 Rat suppr
c	39	33	3.4	237	5	AAH65905	Aah65905 C glutami
c	40	33	3.4	237	8	ACA00255	Aca00255 C. glutam
c	41	32.8	3.4	1221	4	AAS52633	Aas52633 E. coli D
c	42	32.8	3.4	1221	8	ACA32665	Aca32665 Prokaryot
c	43	32.8	3.4	1221	13	ADT48824	Adt48824 Bacterial
	44	32.6	3.4	467	3	AAC07790	Aac07790 Human sec
	45	32.6	3.4	1813	10	ADF81771	Adf81771 Leukaemia

X NO PD 11/02

PD 2/03

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OM nucleic - nucleic search, using sw model

Run on: April 15, 2005, 11:21:35 ; Search time 4168 Seconds  
(without alignments)  
11125.634 Million cell updates/sec

Title: US-10-616-309-3  
Perfect score: 957  
Sequence: 1 atgaagcaactttggtttgc.....agttcggggcagcgcaatga 957

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	957	100.0	957	6	CQ759953	CQ759953 Sequence
2	957	100.0	1661	1	ECU37455	U37455 Escherichia
3	957	100.0	3192	1	ECU37089	U37089 Escherichia

11/24x  
10/25x  
X  
App1  
knockout  
knockout

c	4	957	100.0	12767	1	AE015278	101 2002 X 1995	AE015278 Shigella	
c	5	957	100.0	29254	1	ECOK12RIII		D64044 Escherichia	← doing
c	6	957	100.0	110000	1	U00096_26		Continuation (27 o	
c	7	957	100.0	110000	1	U00096_27		Continuation (28 o	
c	8	957	100.0	290380	1	AE016987		AE016987 Shigella	Genome
c	9	953.8	99.7	10208	1	AE005487	2001 *	AE005487 Escherich	SED.
c	10	953.8	99.7	270365	1	AP002562		AP002562 Escherich	
c	11	931.4	97.3	300099	1	AE016764		AE016764 Escherich	
c	12	677	70.7	145050	1	AL627275	200 p	AL627275 Salmonell	
	13	677	70.7	300431	1	AE016835	2003	AE016835 Salmonell	
	14	672.2	70.2	13311	1	STAF001386	1997	AF001386 Salmonell	
	15	672.2	70.2	13311	6	AX191732		AX191732 Sequence	not overexpressed
c	16	672.2	70.2	22108	1	AE008819		AE008819 Salmonell	
	17	638.8	66.8	1122	6	BD248394		BD248394 Gene part	
	18	556.8	58.2	1041	6	AR387875		AR387875 Sequence	
	19	380.8	39.8	4819	1	AY098586		AY098586 Yersinia	
	20	355.2	37.1	10886	1	AE013731		AE013731 Yersinia	
	21	355.2	37.1	258050	1	AJ414153		AJ414153 Yersinia	
	22	355.2	37.1	290294	1	AE017136		AE017136 Yersinia	
c	23	353.6	36.9	110000	1	BX936398	34	Continuation (35 o	
c	24	319.6	33.4	110000	1	BX950851	36	Continuation (37 o	
c	25	257.8	26.9	348505	1	BX571870		BX571870 Photorhab	
	26	257.8	26.9	349980	6	AX770909		AX770909 Sequence	
	27	228.4	23.9	3545	1	PHRRPOE		L41667 Photobacter	
	28	228.4	23.9	3545	1	PHRRPOEA		L41688 Photobacter	
c	29	226.8	23.7	349814	1	CR378673		CR378673 Photobact	
c	30	202.4	21.1	296650	1	AP005082		AP005082 Vibrio pa	
c	31	194.8	20.4	12162	1	AE004316		AE004316 Vibrio ch	
	32	191.2	20.0	1020	6	AR378439		AR378439 Sequence	
c	33	178.4	18.6	248650	1	AP005341		AP005341 Vibrio vu	
	34	167.2	17.5	300732	1	AE016802		AE016802 Vibrio vu	
	35	136.6	14.3	10631	1	U32746		U32746 Haemophilus	
	36	136.6	14.3	106645	6	CQ873068		CQ873068 Sequence	
	37	136.6	14.3	110000	6	BD426631	06	Continuation (7 of	
	38	136.6	14.3	110000	6	AR274513	06	Continuation (7 of	
	39	136.6	14.3	110000	6	AR541453	06	Continuation (7 of	
c	40	122	12.7	11975	1	AE006215		AE006215 Pasteurel	
	41	100	10.4	100	6	AX999583		AX999583 Sequence	
	42	100	10.4	100	6	AX999584		AX999584 Sequence	
	43	100	10.4	100	6	AX999585		AX999585 Sequence	
	44	81	8.5	831	1	ECU10148		U10148 Escherichia	
	45	79	8.3	110000	1	AE016827	21	Continuation (22 o	

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OM nucleic - nucleic search, using sw model

Run on: April 15, 2005, 11:28:45 ; Search time 207 Seconds  
(without alignments)  
7564.816 Million cell updates/sec

Title: US-10-616-309-3  
Perfect score: 957  
Sequence: 1 atgaagcaacttttggtttgc.....agttcggggcagcgcaatga 957

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	556.8	58.2	1041	4	US-09-489-039A-4604	Sequence 4604, Ap
2	191.2	20.0	1020	4	US-09-543-681A-3445	Sequence 3445, Ap
3	136.6	14.3	1830121	4	US-09-557-884-1	Sequence 1, Appli
4	136.6	14.3	1830121	4	US-09-643-990A-1	Sequence 1, Appli
5	37.6	3.9	1800	1	US-08-260-202A-10	Sequence 10, Appl
6	37.6	3.9	1800	1	US-08-017-114-10	Sequence 10, Appl
7	37.6	3.9	1800	3	US-08-505-307-10	Sequence 10, Appl
8	37.6	3.9	1800	3	US-09-609-151A-10	Sequence 10, Appl
9	37.6	3.9	1800	5	PCT-US94-02034-10	Sequence 10, Appl
10	36	3.8	1065	4	US-09-252-991A-13070	Sequence 13070, A
c 11	36	3.8	1308	4	US-09-252-991A-12869	Sequence 12869, A

*Conflict*  
*PCT*

*PF 11/00*  
*PF 4/00*  
*Haeem*

*668578 nul*

*6610836*  
*6605709*  
*11/14/03*  
*6506581*

	12	35.2	3.7	601	4	US-09-949-016-193470	Sequence 193470,
c	13	35.2	3.7	268449	4	US-09-949-016-17244	Sequence 17244, A
	14	34.4	3.6	399	4	US-09-621-976-8976	Sequence 8976, Ap
	15	34.2	3.6	254405	4	US-09-949-016-14381	Sequence 14381, A
c	16	33.2	3.5	1882	1	US-08-696-349-1	Sequence 1, Appli
c	17	33.2	3.5	1882	5	PCT-US96-13156-1	Sequence 1, Appli
c	18	32.8	3.4	1788	4	US-09-634-238-184	Sequence 184, App
	19	32.6	3.4	467	4	US-09-513-999C-11865	Sequence 11865, A
	20	32.6	3.4	7218	1	US-08-232-463-14	Sequence 14, Appl
	21	32.6	3.4	85122	4	US-09-949-016-14693	Sequence 14693, A
	22	32.6	3.4	119214	4	US-09-949-016-12507	Sequence 12507, A
c	23	32.2	3.4	861	4	US-09-134-000C-507	Sequence 507, App
c	24	32	3.3	505	4	US-09-621-976-15639	Sequence 15639, A
c	25	32	3.3	1152	4	US-09-252-991A-7217	Sequence 7217, Ap
c	26	32	3.3	1389	4	US-09-252-991A-7279	Sequence 7279, Ap
	27	32	3.3	1428	4	US-09-252-991A-7419	Sequence 7419, Ap
c	28	31.8	3.3	1305	4	US-09-248-796A-1639	Sequence 1639, Ap
	29	31.8	3.3	38584	3	US-09-453-702B-50	Sequence 50, Appl
c	30	31.8	3.3	44836	4	US-09-949-016-14867	Sequence 14867, A
c	31	31.6	3.3	370	4	US-09-621-976-15655	Sequence 15655, A
c	32	31.6	3.3	370	4	US-09-621-976-15656	Sequence 15656, A
c	33	31.6	3.3	371	4	US-09-621-976-15654	Sequence 15654, A
c	34	31.6	3.3	373	4	US-09-621-976-15652	Sequence 15652, A
	35	31.6	3.3	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	36	31.6	3.3	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	37	31.2	3.3	18324	4	US-09-902-540-1196	Sequence 1196, Ap
c	38	31.2	3.3	319608	4	US-09-539-333D-1	Sequence 1, Appli
c	39	31.2	3.3	319608	4	US-09-679-409-1	Sequence 1, Appli
c	40	31	3.2	498	4	US-09-621-976-1174	Sequence 1174, Ap
c	41	31	3.2	2229	4	US-09-196-270-22	Sequence 22, Appl
c	42	31	3.2	2603	4	US-09-620-312D-903	Sequence 903, App
c	43	31	3.2	76269	4	US-09-949-016-14603	Sequence 14603, A
	44	30.8	3.2	1141	4	US-09-806-708B-22	Sequence 22, Appl
c	45	30.8	3.2	5099	4	US-09-887-052-1	Sequence 1, Appli

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OM nucleic - nucleic search, using sw model

Run on: April 15, 2005, 11:50:01 ; Search time 599 Seconds  
(without alignments)  
9692.559 Million cell updates/sec

Title: US-10-616-309-3  
Perfect score: 957  
Sequence: 1 atgaagcaacttttggtttgc.....agttcggggcagcgcaatga 957

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5622541 seqs, 3033355566 residues

Total number of hits satisfying chosen parameters: 11245082

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_NA:\*  
1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*  
10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*  
12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*  
14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*  
15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*  
16: /cgn2\_6/ptodata/2/pubpna/US10D\_PUBCOMB.seq:\*  
17: /cgn2\_6/ptodata/2/pubpna/US10E\_PUBCOMB.seq:\*  
18: /cgn2\_6/ptodata/2/pubpna/US10F\_PUBCOMB.seq:\*  
19: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
20: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*  
21: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*  
22: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result		Query				Description
No.	Score	Match	Length	DB	ID	
1	957	100.0	957	19	US-10-616-309-3	Sequence 3, Appli
2	638.8	66.8	1122	16	US-10-342-224-75X	Sequence 75, Appl
3	136.6	14.3	1830121	17	US-10-329-670-1X	Sequence 1, Appli
4	136.6	14.3	1830121	18	US-10-158-865-1	Sequence 1, Appli
5	38	4.0	951	17	US-10-369-493-35958	Sequence 35958, A
c 6	37.8	3.9	763	17	US-10-369-493-35488	Sequence 35488, A
c 7	37.8	3.9	763	17	US-10-369-493-38254	Sequence 38254, A
8	36.6	3.8	625	14	US-10-123-155-70	Sequence 70, Appl
9	36.6	3.8	625	15	US-10-146-731-70	Sequence 70, Appl
10	36.6	3.8	625	15	US-10-140-472-70	Sequence 70, Appl
11	36.6	3.8	625	15	US-10-141-761-70	Sequence 70, Appl
12	36.6	3.8	625	16	US-10-142-885-70	Sequence 70, Appl
13	36.6	3.8	625	16	US-10-158-790-70	Sequence 70, Appl
14	36.6	3.8	625	17	US-10-137-871-70	Sequence 70, Appl
15	36.6	3.8	625	17	US-10-140-923-70	Sequence 70, Appl
16	36.6	3.8	625	17	US-10-141-756-70	Sequence 70, Appl
17	36.6	3.8	625	17	US-10-141-759-70	Sequence 70, Appl
18	36.6	3.8	625	17	US-10-140-805-70	Sequence 70, Appl
19	36.6	3.8	625	17	US-10-140-864-70	Sequence 70, Appl
20	36.6	3.8	625	17	US-10-142-426-70	Sequence 70, Appl
21	35.8	3.7	3309400	9	US-09-738-626-1	Sequence 1, Appli
c 22	34.6	3.6	33578	17	US-10-085-117-238	Sequence 238, App
c 23	34.4	3.6	79256	18	US-10-322-281-167	Sequence 167, App
24	34.2	3.6	421	10	US-09-918-995-17765	Sequence 17765, A
25	34.2	3.6	400660	18	US-10-388-838-68	Sequence 68, Appl
26	33.6	3.5	2004	17	US-10-424-599-37007	Sequence 37007, A
c 27	33.6	3.5	168407	18	US-10-322-281-305	Sequence 305, App
28	33.4	3.5	2256646	18	US-10-470-565-1	Sequence 1, Appli
c 29	33.2	3.5	317	18	US-10-767-795-971	Sequence 971, App
c 30	33	3.4	237	9	US-09-738-626-940	Sequence 940, App
31	33	3.4	462	17	US-10-242-535A-44051	Sequence 44051, A
32	33	3.4	462	17	US-10-085-783A-44051	Sequence 44051, A
c 33	33	3.4	576	13	US-10-027-632-321958	Sequence 321958,
c 34	33	3.4	576	17	US-10-027-632-321958	Sequence 321958,
c 35	32.8	3.4	1221	9	US-09-815-242-6270	Sequence 6270, Ap
c 36	32.8	3.4	1221	17	US-10-369-493-47262	Sequence 47262, A
c 37	32.8	3.4	1221	17	US-10-282-122A-20535	Sequence 20535, A
c 38	32.8	3.4	2471	18	US-10-739-930-4858	Sequence 4858, Ap
39	32.6	3.4	1963	9	US-09-925-300-524	Sequence 524, App
40	32.6	3.4	5632	14	US-10-198-846-13537	Sequence 13537, A
c 41	32.6	3.4	7047	18	US-10-450-224-1	Sequence 1, Appli
42	32.6	3.4	358246	17	US-10-292-798-1095	Sequence 1095, Ap
c 43	32.4	3.4	877	17	US-10-282-122A-9278	Sequence 9278, Ap
c 44	32.4	3.4	1242	17	US-10-425-114-5071	Sequence 5071, Ap
45	32.4	3.4	1494	17	US-10-369-493-35952	Sequence 35952, A



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OM nucleic - nucleic search, using sw model

Run on: April 15, 2005, 11:27:46 ; Search time 3098 Seconds  
(without alignments)  
11758.394 Million cell updates/sec

Title: US-10-616-309-3  
Perfect score: 957  
Sequence: 1 atgaagcaacttttggtttgc.....agttcggggcagcgcaatga 957

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_htc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			% Query				ID	Description
	No.	Score	Match	Length	DB			
c	1	224.8	23.5	535	9	CL667196	CL667196	PRI0154b_
	2	191.4	20.0	798	9	CL679590	CL679590	PRI0126c_
c	3	119.8	12.5	552	8	AQ990079	AQ990079	Rfc00790_
	4	37.6	3.9	928	9	CNS04AQA	AL282187	Tetraodon
	5	36.6	3.8	464	7	CN816649	CN816649	HRO4523_C
	6	36.6	3.8	1289	5	BU305940	BU305940	603612614
	7	36.6	3.8	1378	8	CC260215	CC260215	CH261-1C2
	8	36.2	3.8	589	5	BQ380762	BQ380762	kk30e04.y

c	9	36.2	3.8	662	5	BQ458073	BQ458073	ko55f03.y
c	10	36.2	3.8	674	5	BQ274578	BQ274578	ko53f02.y
c	11	36.2	3.8	675	5	BQ458055	BQ458055	ko55d05.y
c	12	36.2	3.8	687	5	BQ274580	BQ274580	ko53f06.y
	13	36	3.8	902	6	CA789600	CA789600	AGENCOURT
	14	35.6	3.7	1624	3	CR731608	CR731608	Tetraodon
c	15	35.4	3.7	496	4	BJ305705	BJ305705	BJ305705
	16	35.4	3.7	584	4	BJ322990	BJ322990	BJ322990
	17	35.4	3.7	610	4	BJ311291	BJ311291	BJ311291
c	18	35.4	3.7	649	2	BE442850	BE442850	WHE1107_F
	19	35.4	3.7	679	4	BJ311074	BJ311074	BJ311074
	20	35.2	3.7	313	8	AQ452178	AQ452178	HS_5092_A
c	21	35	3.7	395	9	CNS07H3T	AL610571	Anopheles
	22	35	3.7	484	8	BH377963	BH377963	AG-ND-155
c	23	35	3.7	695	8	BH369286	BH369286	AG-ND-163
c	24	35	3.7	759	7	CK177093	CK177093	EST766413
	25	35	3.7	812	7	CK177094	CK177094	EST766414
c	26	35	3.7	919	9	CNS01JWH	AL147586	Anopheles
	27	34.8	3.6	372	7	CF689180	CF689180	CCAAW76TR
	28	34.8	3.6	649	7	CF682789	CF682789	CCACR84TR
	29	34.8	3.6	662	1	AI392092	AI392092	NCM9C5T3
	30	34.8	3.6	722	7	CO047190	CO047190	Lr_AT1CF_
	31	34.8	3.6	728	7	CF716039	CF716039	CCAHS81TR
	32	34.8	3.6	748	7	CF710464	CF710464	CCAAAY96TR
	33	34.8	3.6	765	7	CF714916	CF714916	CCADG32TR
	34	34.8	3.6	774	7	CF722374	CF722374	CCAAO76TR
	35	34.8	3.6	793	7	CF705374	CF705374	CCAGG04TR
	36	34.8	3.6	838	7	CF722152	CF722152	CCAGO08TR
	37	34.8	3.6	858	7	CF694365	CF694365	CCAGV55TR
	38	34.8	3.6	869	7	CF676826	CF676826	CAHN73TR
c	39	34.6	3.6	295	5	BQ125873	BQ125873	ko46f03.y
c	40	34.6	3.6	328	7	CN243461	CN243461	EST009337
	41	34.6	3.6	331	7	H92696	H92696	yt90d02.r1
c	42	34.6	3.6	342	5	BQ493687	BQ493687	EST02853
c	43	34.6	3.6	359	7	CN242898	CN242898	EST008770
c	44	34.6	3.6	459	5	BQ493062	BQ493062	EST02228
c	45	34.6	3.6	613	4	BG494351	BG494351	602539306